



#12

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/381,497A

DATE: 05/21/2001 TIME: 11:16:56

Input Set : A:\-317-1.app

Output Set: N:\CRF3\05212001\I381497A.raw

ENTERED SEQUENCE LISTING (1) GENERAL INFORMATION: (i) APPLICANT: FitzGerald, David 7 Pastan, Ira Mansfield, Elizabeth 8 Kreitman, Robert q (ii) TITLE OF INVENTION: Recombinant Antibodies and 11 12 Immunoconjugates Targeted to CD-22 Bearing Cells and 13 (iii) NUMBER OF SEQUENCES: 15 15 17 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Townsend and Townsend and Crew LLP 18 19 (B) STREET: Two Embarcadero Center, Eighth Floor 20 (C) CITY: San Francisco (D) STATE: California 21 22 (E) COUNTRY: USA 23 (F) ZIP: 94111-3834 25 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk 26 (B) COMPUTER: IBM PC compatible 27 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 31 (vi) CURRENT APPLICATION DATA: C--> 32 (A) APPLICATION NUMBER: US/09/381,497A C--> 33 (B) FILING DATE: 21-May-2001 34 (C) CLASSIFICATION: 40 (vii) PRIOR APPLICATION DATA: 37 (A) APPLICATION NUMBER: WO PCT/US98/05453 38 (B) FILING DATE: 19-MAR-1998 41 (A) APPLICATION NUMBER: US 60/041,437 42 (B) FILING DATE: 20-MAR-1997 44 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Weber, Ellen Lauver 45 (B) REGISTRATION NUMBER: 32,762 46 47 (C) REFERENCE/DOCKET NUMBER: 015280-317100US (ix) TELECOMMUNICATION INFORMATION: 49 50 (A) TELEPHONE: (415) 576-0200 51 (B) TELEFAX: (415) 576-0300 54 (2) INFORMATION FOR SEQ ID NO: 1: 56 (i) SEQUENCE CHARACTERISTICS: 57 (A) LENGTH: 369 base pairs (B) TYPE: nucleic acid 58 (C) STRANDEDNESS: single 59 60 (D) TOPOLOGY: linear W--> 62 (ii) MOLECULE TYPE: DNA (ix) FEATURE: 65

(A) NAME/KEY: CDS

66

RAW SEQUENCE LISTING DATE: 05/21/2001 PATENT APPLICATION: US/09/381,497A TIME: 11:16:56

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68 71		/vi	•	O) OI									i nec	avy (JIIali		
	GAA	•											AAG	ССТ	GGA	GGG	48
	Glu																
75	1		· · · ·	200	5	010		011	0-1	10					15	V-1	
	TCC	CTG	AAA	CTC	_	TGT	GCA	GCC	TCT		TTC	GCT	TTC	AGT		TAT	96
	Ser																
79			•	20		•			25	•				30		-	
81	GAC	ATG	TCT	TGG	GTT	CGC	CAG	ACT	CCG	GAG	AAG	AGG	CTG	GAG	TGG	GTC	144
	Asp																
83	_		35					40					45				
85	GCA	TAC	ATT	AGT	AGT	GGT	GGT	GGT	ACC	ACC	TAC	TAT	CCA	GAC	ACT	GTG	192
86	Ala	Tyr	Ile	Ser	Ser	Gly	Gly	Gly	Thr	Thr	Tyr	Tyr	Pro	Asp	Thr	Val	
87		50					55					60					
	AAG																240
90	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn		Ļys	Asn	Thr	Leu		
91						70					75					80	
	CTG																288
	Leu	Gln	Met	Ser		Leu	Lys	Ser	Glu	-	Thr	Ala	Met	Tyr		Cys	
9.5					85					90	~~~				95		226
	GCA																336
	Ala	Arg	His		GLY	Tyr	GTĀ	Ser		Tyr	GIY	val	Leu		Ala	Tyr	
99	1 maa		י מיט	100	3 00	. cmc	· cmc		105	, m.c.a				110			369
TO.	l TGG	, 666	. L.A.F														
10											_						303
	2 Trp		glr Glr	Gly				Thi	Val		_						303
10	2 Trp	Gly	Glr 115	Gly	Thr	Leu	ı Val	Thi 120	Val		_						303
10 10	2 Trp 3 5 (2)	Gl _y	Glr 115 FORMA	Gly 5 ATION	Thr FOF	: Leu R SEQ	val	Th: 120 NO:	Va]) 2:		_						303
10 10 10	2 Trp 3 5 (2) 3	Gl _y	Glr 115 FORMA () SE	Gly TION QUEN	Thr FOF	Leu R SEC	val DID CTE	Thi 120 NO: RISTI	Val) 2: [CS:	. Ser	_						303
10 10	2 Trp 3 6 (2) 3	Gl _y	Glr 115 FORMA () SE	Gly TION COUEN A) I	Thr FOF ICE C ENGT	Leu R SEC CHARA CH: 1	Val DID CTER	Thi 120 NO: RISTI	Val) 2: [CS:	. Ser	_						303
10 10 10 10	2 Trp 3 5 (2) 3 9	Gl _y	Glr 115 FORMA L) SE (Gly TION QUEN A) I B) T	Thi FOF ICE C ENGT	E Leu R SEQ CHARA CH: 1 ami	Val O ID ACTEI 123 a .no a	Thi 120 NO: RISTI mino	Val) 2: [CS:	. Ser	_						303
10: 10: 10: 11:	2 Trp 3 6 (2) 3 9 0	OGLY INF	Glr 115 FORMA () SE ()	Gly TION COUEN A) I	Thi FOF ICE C ENGT YPE:	E Leu CHARA CH: 1 ami LOGY:	I Vall CTER 123 a no a	The 120 NO: RISTI mind acid near	Val 2: CS: aci	. Ser	_						303
10: 10: 10: 10: 11:	2 Trp 3 (2) 5 (2) 6 (2) 1 (2)	INE (ii	Glr 115 FORMA () SE () ()	Gly TION CQUEN A) I B) I	Thr I FOF ICE C LENGT LYPE: COPOL	E Leu R SEQ CHARA TH: I ami LOGY:	Vallo	The 120 NO: RISTI amino acid acar bteir	Val) 2: ICS: Daci	. Ser	Ala	1					303
10: 10: 10: 11: 11: 11:	2 Trp 3 (2) 8 (2) 1 (2) 1 (3)	INE (ii (xi	Glr 115 FORMA () SE () () ()	Gly TION QUEN A) I B) I DLECU	Thr I FOF ICE C ENGT YPE: YOPOI ILE I	E Leu CHARA CH: 1 ami LOGY: CYPE:	Vallo	Thr 120 NO: RISTI mino ncid near oteir	Val) 2: ICS: o aci	. Sei .ds	Ala	a 2 :	L Lys	s Pro	o Gly	7 Gly	
10: 10: 10: 11: 11: 11:	2 Trp 3 (2) 8 (2) 1 (3) 1 (3) 7 Glu	INE (ii) (xi) (Val)	Glr 115 FORMA () SE () () ()	Gly TION QUEN A) I B) I DLECU	Thr I FOF ICE C ENGT YPE: YOPOI ILE I	R SECHARA CH: 1 ami LOGY: CYPE: CESCF	Vallo	Thr 120 NO: RISTI mino ncid near oteir	Val) 2: ICS: o aci	. Sei .ds	Ala NO: 2	a 2 :	L Lys	s Pro	o Gl ₃		
10: 10: 10: 11: 11: 11: 11:	2 Trp 3 (2) 3 (2) 1 (3) 5 (3) 7 Glu 3 1	INE (ii (xi Val	7 Glr 115 FORMA 1) SE ((((L) MC L) SE Glr	ATION EQUEN (A) I (B) I (D) I DLECU EQUEN	Thi FOF LENGT LYPE: COPOL LE T ICE C	E Leu R SEC CHARA TH: 1 ami LOGY: TYPE: DESCR Glu	O Val	Thr 120 NO: RISTI mind cid lear oteir ON:	Yall) 2: ICS: Caci	. Ser .ds ID N Gly	O: 2	i 2: 1 Val			15		
10: 10: 10: 11: 11: 11: 11:	2 Trp 3 (2) 6 (2) 6 (2) 6 (3) 7 Glu 7 Glu 8 1	INE (ii (xi Val	7 Glr 115 FORMA 1) SE ((((L) MC L) SE Glr	ATION EQUEN (A) I (B) I (D) I DLECU EQUEN	Thir I FOF LENGT TYPE: TOPOL ILE T ICE D Val	E Leu R SEC CHARA TH: 1 ami LOGY: TYPE: DESCR Glu	O Val	Thr 120 NO: RISTI mind cid lear oteir ON:	Yall) 2: ICS: Caci	. Ser .ds ID N Gly 10	O: 2	i 2: 1 Val			15 11e	5	
10: 10: 10: 11: 11: 11: 11: 12: 12: 12:	2 Trp 3 6 (2) 8 9 1 1 7 Glu 8 1 1 Ser 1 8 Asp	INE (ii (xi Val	Glr	TION ATION ATION AQUEN (A) I (B) I DLECU QUEN 1 Leu 20 Trp	Thir FOR LENGT TYPE: TOPOI ILE T ICE I Val	R SECHARA CH: 1 ami LOGY: CYPE: DESCRIPTION Glui CYS	I Val	Thr 120 NO: RISTI mino ncid near oteir ON: Gly	Yall) 2: CS: CS: SEQ Gly Ser 25	.ds ID N Gly 10	TO: 2 Leu	a 2: 1 Val ≥ Ala	ı Phe	Sei 30 i Gli	15 116	5	
10: 10: 10: 11: 11: 11: 11: 12: 12: 12: 12:	2 Trp 3 6 (2) 8 9 1 1 7 Glu 8 1 9 Ser 1 8 Asp	INE (ii (xi (xi Val	Glr Glr FORMA () SE () () () () SE Glr 1 Lys	A Gly ATION CQUEN A) I B) I D) I D) ECUEN A Leu S Leu Trp	Thr I FOR ICE C ENGT TYPE: TOPOI ICE I ICE I I Val	R SECHARA CH: 1 ami LOGY: YPE: DESCR Glu CYS	P Value Valu	Thr 120 NO: RISTI mino acid mear bteir CON: Gly	Yall	.ds ID N Gly Gly Gly Gly	NO: 2 V Leu) V Phe	2: 1 Val 2 Ala 3 Arç	Phe Leu 45	e Sei 3(i Gli	15 F Ile D I Tr	Tyr Val	
10.1 10.0 10.0 11.0 11.1 11.1 11.1 12.0 12.1 12.1	2 Trp 3 6 (2) 8 9 1 1 7 Glu 3 1 5 Ser 1 1 1 1 1 5 Ala	INF (ii) (xi) (xa) Val Let Met	Glr 115 FORMA L) SE (((L) MC L) SE Glr Lys Lys Lys Lys Lys Lys	A Gly ATION CQUEN A) I B) I D) I D) ECUEN A Leu S Leu Trp	Thr I FOR ICE C ENGT TYPE: TOPOI ICE I ICE I I Val	R SECHARA CH: 1 ami LOGY: YPE: DESCR Glu CYS	o Val	Thr 120 NO: RISTI minor icid icear oteir CON: GON: GON: GON: GON: GON: GON: GON: GON: GON: GON: GON:	Yall	.ds ID N Gly Gly Gly Gly	NO: 2 V Leu) V Phe	2: 1 Val 2 Ala 3 Arç 7 Tyr	Leu 45 Pro	e Sei 3(i Gli	15 F Ile D I Tr	5 e Tyr	
100 100 110 111 111 112 122 122 123 124 127	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 Ser 1 1 8 Asp 1 7	O Gly INF (ii (xi Val Leu Met	Glr Glr Glr Glr Glr Glr Glr Glr Glr Glr	A Gly ATION CQUEN A) I B) I D) I D) LECU CQUEN A Leu 20 Trp B S Ser	Third FOR THE STATE OF THE STAT	S SECTION SECT	o Val	Thr 120 NO: RISTI minorated con: CON	Yall 2: CS: SEQ Gly Ser 25 Thr	. Ser .ds .ds .Gly .Gly .Gly	NO: 2 Leu Phe Lys	2: 1 Val 2: Ala 3 Arç 7 Tyr 60	Leu 45 Pro	Ser 3(I Glu Asp	15 Tle Trp	Tyr Val	
100 100 110 111 111 112 123 124 126 127 128	2 Trp 3 6 (2) 8 9 1 1 7 Glu 8 8 1 8 Ser 1 1 8 Asp 1 1 9 Lys	INE (iii (xi (xi Val) Leu Met	Glr Glr Glr Glr Glr Glr Glr Glr Glr Glr	A Gly ATION CQUEN A) I B) I D) I D) LECU CQUEN A Leu 20 Trp B S Ser	Third FOR THE STATE OF THE STAT	S SECTION SECT	O Value Valu	Thr 120 NO: RISTI minor icid icear oteir CON: Gly i Ala Thr 40 r Gly	Yall 2: CS: SEQ Gly Ser 25 Pro	. Ser .ds .ds .Gly .Gly .Gly	O: 2 Leu Phe Lys	2: 1 Val 2 Ala 3 Arç 6 Tyr 6 C	Leu 45 Pro	Ser 3(I Glu Asp	15 Tle Trp	Tyr Val Val	
100 100 100 110 111 111 112 123 124 126 127 128 130	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 1 8 Asp 1 1 6 Ala 7 9 Lys	INE (iii (xii Val	Glr (() () () () () () () () () () () () ()	A Gly ATION CQUEN A) I B) I CD) I CQUEN A Leu 20 CTrp CS Ser	This FOR THE STATE OF THE THE SERVICE OF THE SERVIC	S SECTION SECT	Value	Thm 120 NO: RISTI maincacid hear oteir CON: Gly Ala Thr 40 Gly; Arg	Value	. Ser ds .ds .ID N .Gly .10 .Gly .Gly .Thr	O: 2 VO: 2 VO: 2 VO: Lev VO: Phe VO: Tyr	2: 1 Val 2 Ala 3 Arg 7 Tyr 60 1 Lys	Leu 45 Pro	Ser 30 1 Glu 5 2 Asp	1! TILE This Let	Tyr Val Val Tyr 80	
100 100 100 111 111 112 120 122 123 124 136 133	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 1 8 Asp 1 1 6 Ala 7 9 Lys 8 Leu	INE (iii (xii Val	Glr (() () () () () () () () () () () () ()	A Gly ATION CQUEN A) I B) I CD) I CQUEN A Leu 20 CTrp CS Ser	This FOR THE SET TO THE	S SECTION SECT	Value	Thm 120 NO: RISTI maincacid hear oteir CON: Gly Ala Thr 40 Gly; Arg	Value	. Ser ds ds ID N Gly 10 Gly 5 Gly 7 Gly 7 Asr	O: 2 O: 2 O: 2 O: 4 O: 5 O: 4 O: 5 O: 4 O: 5 O: 5	2: 1 Val 2 Ala 3 Arg 7 Tyr 60 1 Lys	Leu 45 Pro	Ser 30 1 Glu 5 2 Asp	1! Ile Trp Thi Lei	Tyr Val Tyr 80 Cys	
100 100 100 111 111 112 120 120 120 131 131 131	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 1 8 Asp 1 1 6 Ala 7 9 Lys 2 Leu 8	INE (iii (xii Val	Glr (() () () () () () () () () () () () ()	ATION CQUEN (A) I (B) I (C) I	This FOR THE SET THE S	S SECTION SECT	Value	Thm 120 NO: RISTI main cold dear oteir CON: Gly Ala Thr 40 Gly; Arg	Value	. Ser ds ds ID N Gly 10 Gly 5 Gly 6 Thr	O: 2 VO: 2 V Lev Phe 1 Lys Tyr 1 Ala 75 Thr	2: 1 Val 2: Ala 3 Arg 7 Tyr 60 1 Lys 3 Ala	Leu 45 Pro Asr	Ser 3(1 Glu 5 2 Asp 1 Thr	1! c Ile l Ir l Tr l T	Val Val Tyr 80 Cys	
10 10 10 10 11 11 11 11 12 12 12 12 12 13 13 13 13 13	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 Asp 1 1 6 Ala 7 9 Lys 9 Lys 2 Leu 8 8 Ala	INE (iii (xii Val	Glr (() () () () () () () () () () () () ()	ATION CQUEN (A) I (B) I (C) I	This FOR THE SET TO SET THE SE	S SECTION SECT	Value	Thm 120 NO: RISTI main cold dear oteir CON: Gly Ala Thr 40 Gly; Arg	Value	ds ID N (Gly 10 Gly) Gly Thr Asr 90 Tyr	O: 2 VO: 2 V Lev Phe 1 Lys Tyr 1 Ala 75 Thr	2: 1 Val 2: Ala 3 Arg 7 Tyr 60 1 Lys 3 Ala	Leu 45 Pro Asr	Ser 30 1 Glu 5 D Asr Thr Tyr	1! Ile Ile Tri Tri Lei Tyi 9!	Tyr Val Tyr 80 Cys	
10 10 10 10 11 11 11 11 12 12 12 12 12 13 13 13 13 13 13	2 Trp 3 6 (2) 8 9 1 1 8 7 Glu 8 8 Asp 1 1 6 Ala 7 9 Lys 9 Lys 2 Leu 8 8 Ala	INE (iii (xii Val	Glr 115 FORMA () () () () () () () () () () () () ()	ATION CQUEN (A) I (B) I (C) I	This FOR THE SET THE S	S SECTION SECT	Value	Thin 120 NO: RISTI minor cid dear oteir con: Gly Ala Thin 40 Gly; Ser Ser Ser	Value	ds ID N (Gly 10 Gly 10 Gly 11 Gly 11 Gly 12 Gly 13 Gly 14 Gly 15 Gly 16 Gly 17 Gly 17 Gly 18	O: 2 O: 2 Phe 1 Lys 75 Thr	2: 1 Val 2: Ala 3 Arg 60 1 Lys 3 Ala	Leu 45 Pro Asr	Ser 3(1 Glu 5 2 Asp 1 Thr	1! Ile Tri Tri Thi Lei Tyi 9!	Val Val Tyr 80 Cys	

RAW SEQUENCE LISTING DATE: 05/21/2001 PATENT APPLICATION: US/09/381,497A TIME: 11:16:57

Input Set : A:\-317-1.app

Output Set: N:\CRF3\05212001\I381497A.raw

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139
                 115
                                     120
     142 (2) INFORMATION FOR SEQ ID NO: 3:
              (i) SEQUENCE CHARACTERISTICS:
     145
                   (A) LENGTH: 321 base pairs
     146
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: single
     147
     148
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: DNA
W--> 150
             (ix) FEATURE:
     153
     154
                   (A) NAME/KEY: CDS
     155
                   (B) LOCATION: 1..321
     156
                   (D) OTHER INFORMATION: /product= "RFB4 light chain"
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
     159
     161 GAT ATC CAG ATG ACC CAG ACT ACA TCC TCC CTG TCT GCC TCT CTG GGA
                                                                                 48
     162 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
                           5
                                              10
     165 GAC AGA GTC ACC ATT AGT TGC AGG GCA AGT CAG GAC ATT AGC AAT TAT
                                                                                 96
     166 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
                      20
                                          25
     169 TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT AAA CTC CTG ATC
                                                                                144
     170 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
                 35
                                      40
     173 TAC TAC ACA TCA ATA TTA CAC TCA GGA GTC CCA TCA AGG TTC AGT GGC
                                                                                192
     174 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
                                  55
                                                      60
              50
     177 AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC AAC CTG GAG CAA
                                                                                240
     178 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
                              70
     181 GAA GAT TTT GCC ACT TAC TTT TGC CAA CAG GGT AAT ACG CTT CCG TGG
                                                                                288
     182 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                                              90
                          85
     185 ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA
                                                                                321
     186 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
     187
                     100
                                         105
     190 (2) INFORMATION FOR SEQ ID NO: 4:
              (i) SEQUENCE CHARACTERISTICS:
     192
     193
                   (A) LENGTH: 107 amino acids
                   (B) TYPE: amino acid
    194
     195
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: protein
     197
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
     201 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
                           5
                                              10
    204 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
                     20
                                          25
     207 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
                35
                                      40
    210 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
             50
                                  55
    211
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DATE: 05/21/2001

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PATENT APPLICATION: US/09/381,497A
                                                               TIME: 11:16:57
                      Input Set : A:\-317-1.app
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     213 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
     216 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                                               90
                           85
     219 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                      100
                                          105
     220
     223 (2) INFORMATION FOR SEQ ID NO: 5:
              (i) SEQUENCE CHARACTERISTICS:
     225
     226
                    (A) LENGTH: 4 amino acids
     227
                    (B) TYPE: amino acid
     228
                    (C) STRANDEDNESS:
                    (D) TOPOLOGY: linear
     229
              (ii) MOLECULE TYPE: peptide
     231
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
     234
     236
              Gly Gly Gly Ser
     237
     240 (2) INFORMATION FOR SEQ ID NO: 6:
              (i) SEQUENCE CHARACTERISTICS:
     242
     243
                    (A) LENGTH: 33 base pairs
                    (B) TYPE: nucleic acid
     244
                    (C) STRANDEDNESS: single
     245
     246
                    (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: DNA
W--> 248
     251
              (ix) FEATURE:
     252
                    (A) NAME/KEY: -
     253
                    (B) LOCATION: 1..33
                    (D) OTHER INFORMATION: /note= "RFB4 VH5 heavy chain primer"
     254
     257
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     259 GGACCTCATA TGGAAGTGCA GCTGGTGGAG TCT
                                                                                   33
     262 (2) INFORMATION FOR SEQ ID NO: 7:
     264
              (i) SEQUENCE CHARACTERISTICS:
     265
                    (A) LENGTH: 24 base pairs
     266
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
     267
     268
                    (D) TOPOLOGY: linear
W--> 270
             (ii) MOLECULE TYPE: DNA
     273
             (ix) FEATURE:
     274
                    (A) NAME/KEY: -
     275
                    (B) LOCATION: 1..24
     276
                    (D) OTHER INFORMATION: /note= "gamma-CH1 heavy chain primer"
     279
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                   24
     281 AGCAGATCCA GGGGCCAGTG GATA
     284 (2) INFORMATION FOR SEQ ID NO: 8:
     286
              (i) SEQUENCE CHARACTERISTICS:
     287
                    (A) LENGTH: 54 base pairs
     288
                    (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: single
     289
     290
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: DNA
W--> 292
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DATE: 05/21/2001

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Input Set : A:\-317-1.app Output Set: N:\CRF3\05212001\I381497A.raw 295 (ix) FEATURE: (A) NAME/KEY: -296 297 (B) LOCATION: 1..54 (D) OTHER INFORMATION: /note= "RFB4 VH3 heavy chain primer" 298 301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: 303 AGATCCGCCA CCACCGGATC CGCCTCCGCC TGCAGAGACA GTGACCAGAG TCCC 54 306 (2) INFORMATION FOR SEQ ID NO: 9: 308 (i) SEQUENCE CHARACTERISTICS: 309 (A) LENGTH: 27 base pairs 310 (B) TYPE: nucleic acid 311 (C) STRANDEDNESS: single (D) TOPOLOGY: linear 312 W--> 314 (ii) MOLECULE TYPE: DNA (ix) FEATURE: 317 318 (A) NAME/KEY: ~ 319 (B) LOCATION: 1..27 320 (D) OTHER INFORMATION: /note= "RFB4 VH3 dsFv heavy chain 321 primer" 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: 327 CCGGAAGCTT TTGCAGAGAC AGTGACC 27 330 (2) INFORMATION FOR SEQ ID NO: 10: (i) SEQUENCE CHARACTERISTICS: 333 (A) LENGTH: 28 base pairs 334 (B) TYPE: nucleic acid (C) STRANDEDNESS: single 335 (D) TOPOLOGY: linear 336 (ii) MOLECULE TYPE: DNA W--> 338(ix) FEATURE: 341 342 (A) NAME/KEY: -(B) LOCATION: 1..28 343 344 (D) OTHER INFORMATION: /note= "RFB4 VH dsFv(cys) heavy chain 345 primer" 348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: 28 350 GACCCACTCC AGGCACTTCT CCGGAGTC 353 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: 356 (A) LENGTH: 48 base pairs 357 (B) TYPE: nucleic acid 358 (C) STRANDEDNESS: single (D) TOPOLOGY: linear 359 W--> 361 (ii) MOLECULE TYPE: DNA (ix) FEATURE: 364 365 (A) NAME/KEY: -366 (B) LOCATION: 1..48

(D) OTHER INFORMATION: /note= "RFB4 VL5 light chain primer"

370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: 372 GGTGGCGGAT CTGGAGGTGG CGGAAGCGAT ATCCAGATGA CACAGACT

375 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY DATE: 05/21/2001 PATENT APPLICATION: US/09/381,497A TIME: 11:16:58

Input Set : A:\-317-1.app

Output Set: N:\CRF3\05212001\I381497A.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:62 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:150 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:248 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:270 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:292 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
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L:450 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15